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ABSTRACT

There is growing understanding that the environment plays an important role both in the transmission of antibiotic resistant pathogens and in their evolution. Accordingly, researchers and stakeholders world-wide seek to further explore the mechanisms and drivers involved, quantify risks and identify suitable interventions. There is

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a clear value in establishing research needs and coordinating e orts within and across nations in order to best tackle this global challenge. At an international workshop in late September 2017, scientists from 14 countries with expertise on the environmental dimensions of antibiotic resistance gathered to de ne critical knowledge gaps. Four key areas were identi ed where research is urgently needed: 1) the relative contributions of di erent sources of antibiotics and antibiotic resistant bacteria into the environment; 2) the role of the environment, and particularly anthropogenic inputs, in the evolution of resistance; 3) the overall human and animal health impacts caused by exposure to environmental resistant bacteria; and 4) the e cacy and feasibility of di erent technological, social, economic and behavioral interventions to mitigate environmental antibiotic resistance.[1]

1. Introduction

Addressing the global challenge of antibiotic resistance requires a "one-health perspective" that takes into account the connections between human and animal health and the environment[2] (Robinson et al., 2016). This approach is needed because bacteria and bacterial genes often have the ability to move between all three compartments, in any direction (Forsberg et al., 2012; Martinez, 2018; Woolhouse et al., 2015). Such a strategy has been adopted not only within the Global Action Plan of the WHO (WHO, 2015), but also in regional action plans (EC, 2017), in many national action plans (e.g. (India, 2017; Sweden, 2016), by the pharmaceutical industry (IFPMA, 2016) and in the work of other organizations (Access-to-Medicine-Foundation, 2018; AMR-review, 2016). The role of the environment as a transmission route for many bacterial pathogens has long been recognized, often associated with insu cient sewage infrastructure, fecal contamination of water or organic fertilizers (Allen et al., 2010; Bengtsson-Palme et al., 2018a; Finley et al., 2013; Huijbers et al., 2015; Levin et al., 2014; Pruden et al., 2013). More recently, the understanding has developed that many of the resistance genes that we nd in pathogens today originate from bacteria normally thriving in the environment (D'Costa et al., 2011; Forsberg et al., 2012; Poirel et al., 2008; Potron et al., 2011; Taylor et al., 2011; Wellington et al., 2013). Hence, the environment acts as a dispersal route and reservoir of resistant pathogens, and also as an arena for the evolution of resistance (Fig. 1; Bengtsson-Palme et al. 2018b). This paper identi es key knowledge gaps associated with both of these biological processes (transmission and evolution) and with